

09-616 247

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 22:19:44 ; Search time 36 Seconds
(without alignments)
131.466 Million cell updates/sec

Title: US-09-616-247-4
Perfect score: 81
Sequence: 1 QKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	376	16 Q8XA65	Q8XA65 escherichia
2	81	100.0	376	16 Q8FIC5	Q8FIC5 escherichia
3	81	100.0	376	16 Q7UDU1	Q7UDU1 shigella fl
4	81	100.0	379	2 Q8L3D3	Q8L3D3 colwellia m
5	81	100.0	379	16 Q8ZIM6	Q8ZIM6 yersinia pe
6	81	100.0	386	16 Q83MH4	Q83MH4 shigella fl
7	78	96.3	381	16 Q8DF67	Q8DF67 vibrio vuln
8	78	96.3	381	16 Q87RX2	Q87RX2 vibrio para
9	77	95.1	331	2 Q93S23	Q93S23 rhizobium t
10	77	95.1	379	16 Q92T07	Q92T07 rhizobium m
11	73	90.1	376	16 Q98D02	Q98D02 rhizobium l
12	73	90.1	377	16 Q8YE77	Q8YE77 brucella me
13	73	90.1	377	16 Q8FXK1	Q8FXK1 brucella su
14	72	88.9	384	16 Q8RB57	Q8RB57 thermococcus
15	70	86.4	377	16 Q7VQJ3	Q7VQJ3 candidatus
16	70	86.4	383	16 Q89AU7	Q89AU7 buchnera ap

17	69	85.2	382	2 Q8KXK6	Q8KXK6 uncultured
18	66	81.5	386	2 Q93R26	Q93R26 tetragnoco
19	65	80.2	374	16 Q8DZ06	Q8DZ06 wiggleswort
20	64	79.0	392	16 Q8RH03	Q8RH03 fusobacteri
21	63	77.8	373	15 Q7WGIS	Q7WGIS bordetella
22	63	77.8	377	15 Q7W520	Q7W520 bordetella
23	63	77.8	385	16 Q7VYV3	Q7VYV3 bordetella
24	63	77.8	389	16 Q835R5	Q835R5 enterococcu
25	62	76.3	380	16 Q87W1P	Q87W1P pseudomonas
26	61	75.5	387	16 Q8XIT1	Q8XIT1 clostridium
27	60	74.1	373	16 Q92J37	Q92J37 rickettsia
28	60	74.1	375	16 Q8PMA9	Q8PMA9 xanthomonas
29	60	74.1	376	2 Q9APF2	Q9APF2 xanthomonas
30	60	74.1	376	16 Q8PAX8	Q8PAX8 xanthomonas
31	60	74.1	391	16 Q7UM96	Q7UM96 rhodospirill
32	59	72.8	380	16 Q8XM41	Q8XM41 ralstonia s
33	58	71.6	375	16 Q88DU3	Q88DU3 pseudomonas
34	58	71.6	379	2 Q93Q66	Q93Q66 lactococcus
35	58	71.6	456	10 Q8LEU4	Q8LEU4 arabidopsis
36	57	70.4	188	3 Q8NKS8	Q8NKS8 paracoccidi
37	57	70.4	371	16 Q81LS3	Q81LS3 bacillus an
38	57	70.4	371	16 Q818F0	Q818F0 bacillus ce
39	56	69.1	372	16 Q8CWT2	Q8CWT2 streptococc
40	56	69.1	377	16 Q8DWH2	Q8DWH2 streptococc
41	56	69.1	378	2 Q9PAX29	Q9PAX29 streptococc
42	56	69.1	378	16 Q93YCG	Q93YCG streptococc
43	56	69.1	378	16 Q8NZM7	Q8NZM7 streptococc
44	56	69.1	378	16 Q879J5	Q879J5 streptococc
45	56	69.1	379	16 Q8E7Q7	Q8E7Q7 streptococc

ALIGNMENTS

RESULT 1

ID Q8XA65 PRELIMINARY; PRT; 376 AA.
AC Q8XA65;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chapterone with DnaK, heat shock protein (DnaK protein).
GN DnaK OR 20015 OR ECS0015.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boulton A., Shao Y., Miller L.,
RA Grobbeck E.V., Davis N.W., Lim A., Dimlanta E.T., Potamoules K.,
RA Apodaca J., Anantharaman T.S., Iln J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=O157:H7 / RUMD 0509952;
RC MEDLINE=21156231; PubMed=11258796;
RX Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Hattori M., Shinagawa H., Ogasawara N., Yasunaga T.,
RA Kudara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AB005178; AAC54315.1; -;
DR EMBL; AP002550; BAB33438.1; -;
DR PIR; G85481; G85481.

DR PIR; G90630; G90630.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C_1.
 DR Pfam; PF00684; DnaJ_CXXCXG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 2.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS50076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXG; 1.
 DR Heat shock; Complete proteome.
 KW SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 81; DB 16; Length 376;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 2
 Q8FLCS PRELIMINARY; PRT; 376 AA.
 AC O8FLCS;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DE Chapterone protein dnaJ.
 GN DnaJ OR C0020.
 OS Escherichia coli 06.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=06.HI / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raslo D., Buckles E.L., Hou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AB016755; AAN78520.1; -.
 DR PIR; G85481; G85481.
 DR PIR; G90630; G90630.
 DR GO; GO:0003754; F:chaperone activity; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C_1.
 DR Pfam; PF00684; DnaJ_CXXCXG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ_1.
 DR PROSITE; PS00190; CYTOCHROME_C; 2.

DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS50076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXG; 1.
 DR Complete proteome.
 KW SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 81; DB 16; Length 376;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 3
 Q7UDU1 PRELIMINARY; PRT; 376 AA.
 AC Q7UDU1;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DE Chapterone with DnaK, heat shock protein.
 GN DnaJ OR S0015.
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
 RX MEDLINE=22590274; PubMed=12704152;
 RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
 RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
 RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
 RA Schwartz D.C., Blattner F.R.;
 RT "Complete genome sequence and comparative genomics of Shigella
 flexneri serotype 2a strain 2457T."
 RT Infect. Immun. 71:2775-2786(2003).
 DR EMBL; AB016978; AAP15561.1; -.
 DR Heat shock.
 KW SEQUENCE 376 AA; 41072 MW; 1B354AC3F9844532 CRC64;

Query Match 100.0%; Score 81; DB 16; Length 376;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAAFE 15
 Db 61 QKRAAYDQYGHAAFE 75

RESULT 4
 Q8LJD3 PRELIMINARY; PRT; 379 AA.
 AC Q8LJD3;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Heat shock protein 40.
 GN DnaJ.
 OS Colwellia maris (Vibrio sp. (strain ABF-1)).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Colwellia.
 OX NCBI_TaxID=77524;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamauchi S., Okuyama H., Nishiyama Y., Hayashi H.;
 RT "Cloning and transcriptional regulation of dnaK and dnaJ genes from
 psychrophilic bacterium, Colwellia maris."
 RT Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB084455; BAB91324.2; -.
 DR Heat shock.
 KW

SQ SEQUENCE 379 AA; 40995 MW; 58A2894D13F8E9FA CRC64;
 Query Match 100.0%; Score 81; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
 |||||
 DB 61 OKRAAYDQYGHAAFE 75

RESULT 5
 Q8IME PRELIMINARY; PRT; 379 AA.
 AC Q8IME
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Chaperone protein DnaJ (Chaperone with DnaK, heat shock protein).
 GN DnaJ OR YP00469 OR Y3705.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Farraga A.M.,
 Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 Ralwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
 RA "Genome sequence of Yersinia pestis, the causative agent of plague."
 RT Nature 413:523-527(2001).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Butland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 Fetherston J.D., Ilander L.E., Brubaker R.R., Plano G.V.,
 Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 Perry R.D.;
 RA "Genome sequence of Yersinia pestis KIM."
 RT J. Bacteriol. 184:4601-4611(2002).
 RL EMBL; AJ414142; CAC89325.1; -;
 DR EMBL; AE013974; AAMB7253.1; -;
 DR PIR; AB0058; AB0058.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGXG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pep.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C_1.
 DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR PROSITE; PS00190; CYTOCHROME_C; 2.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS0076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
 KM Heat shock; Complete proteome.
 SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match 100.0%; Score 81; DB 16; Length 379;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
 |||||
 DB 61 OKRAAYDQYGHAAFE 75

RESULT 6
 Q83MH4 PRELIMINARY; PRT; 386 AA.
 AC Q83MH4
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Chaperone with DnaK, heat shock protein.
 GN DnaJ OR SF0015.
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 Sun L., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 Yu J.;
 RA "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157."
 RL Nucleic Acids Res. 30:4432-4441(2002).
 DR EMBL; AE015039; AAN41681.1; -;
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0003773; F:heat shock protein activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGXG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pep.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C_1.
 DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ_1.
 DR PROSITE; PS00190; CYTOCHROME_C; 2.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS0076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
 KM Heat shock; Complete proteome.
 SQ SEQUENCE 386 AA; 42279 MW; 172BC403A6E7D75E CRC64;

Query Match 100.0%; Score 81; DB 16; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
 |||||
 DB 71 OKRAAYDQYGHAAFE 85

RESULT 7
 Q8DF67 PRELIMINARY; PRT; 381 AA.
 AC Q8DF67
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE DnaJ chaperone.
 GN VVI0354.
 OS Vibrio vulnificus.

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016798; AA008881.1; -.
DR GO; GO:0003754; F:Chaperone activity; IEA.
DR GO; GO:0005489; F:Electron transporter activity; IEA.
DR GO; GO:0006118; P:Electron transport; IEA.
DR InterPro; IPR00345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C_1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
DR Complete proteome.
SQ SEQUENCE 381 AA; 41226 MW; 1F0783454AE538A6 CRC64;

Query Match
Best Local Similarity 96.3%; Score 78; DB 16; Length 381;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDYGHAFFE 15
Db 61 OKRAAYDYGHAFFE 75

RESULT 8
ID Q87RX2 PRELIMINARY; PRT; 381 AA.
AC Q87RX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DnaJ protein.
GN VP0654.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; Pubmed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Tijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL; AP005075; BAC58917.1; -.
DR GO; GO:0003754; F:Chaperone activity; IEA.
DR GO; GO:0005489; F:Electron transporter activity; IEA.
DR GO; GO:0006118; P:Electron transport; IEA.
DR InterPro; IPR00345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Complete proteome.
SQ SEQUENCE 331 AA; 35577 MW; B2E6D48E002A2C5 CRC64;
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DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C_1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR PROSITE; PS00190; CYTOCHROME_C; 2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
DR Complete proteome.
SQ SEQUENCE 381 AA; 41026 MW; F1DC4DCB64ACD4C6 CRC64;

Query Match
Best Local Similarity 96.3%; Score 78; DB 16; Length 381;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDYGHAFFE 15
Db 61 OKRAAYDYGHAFFE 75

RESULT 9
ID Q93S23 PRELIMINARY; PRT; 331 AA.
AC Q93S23;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DnaJ protein (fragment).
GN DnaJ.
OS Rhizobium tropici.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=398;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CIAT899;
RA Sanjuan J.;
RT "Bacterial osmotolerance and nitrogen-fixing efficiency in Rhizobium-
RT legume symbiosis.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE DNAJ FAMILY.
DR EMBL; AJ311186; CAC38775.1; -.
DR GO; GO:0003754; F:Chaperone activity; IEA.
DR GO; GO:0005489; F:Electron transporter activity; IEA.
DR GO; GO:0006118; P:Electron transport; IEA.
DR InterPro; IPR00345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_C_1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
DR Chapterone; Repeat.
FT NON_TER 1 1
FT NON_TER 331 331
SQ SEQUENCE 331 AA; 35577 MW; B2E6D48E002A2C5 CRC64;
```

```
Query Match
Best Local Similarity 95.1%; Score 77; DB 2; Length 331;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDYGHAFFE 15
Db 39 OKRAAYDYGHAFFE 53
```

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RESULT 10
Q92T07 ID Q92T07 PRELIMINARY; PRT; 379 AA.
AC Q92T07;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Probable chaperone protein.
GN DnaJ OR R00183 OR SMC02858.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaine V., Maesly D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591782; CAC41570.1; -.
DR GO; GO:0003754; F:chaperone activity; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR00345; CytoC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pdp.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DNABPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Complete proteome.
SQ SEQUENCE 379 AA; 41395 MW; B19165E79BB09465 CRC64;

Query Match 95.1%; Score 77; DB 16; Length 379;
Best Local Similarity 93.3%; Pred. No. 6.2e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 60 QKRAAYDRFGHAAFE 74

RESULT 11
Q98DD2 ID Q98DD2 PRELIMINARY; PRT; 376 AA.
AC Q98DD2;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Heat shock protein, DnaJ.
GN M14755.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303059;
```

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RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003004; BAB51339.1; -.
DR GO; GO:0003754; F:chaperone activity; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR00345; CytoC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pdp.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DNABPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Complete proteome.
SQ SEQUENCE 376 AA; 41201 MW; AFA2EABE4C2186E7 CRC64;

Query Match 90.1%; Score 73; DB 16; Length 376;
Best Local Similarity 86.7%; Pred. No. 0.0003;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db 60 QKRAAYDRFGHAAFE 74

RESULT 12
Q8YE77 ID Q8YE77 PRELIMINARY; PRT; 377 AA.
AC Q8YE77;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Chaperone protein DnaJ.
GN BME12001.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kaparatel V., Redkar R.J., Patra G., Mujir C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elizer P.H., Hagius S., O'Callaghan D., Lelesson J.-O.,
RA Haselkorn R., Kyridides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AF009632; AL53182.1; -.
DR PIR; AC3502; AC3502.
DR GO; GO:0003754; F:chaperone activity; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR00345; CytoC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
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DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR003095; Hsp_DnaJ.
DR Pfam: PF00225; DnaJ_1.
DR Pfam: PF01556; DnaJ_C; 1.
DR Pfam: PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS: PR00625; DnaJPROTEIN.
DR SMART: SM00271; DnaJ_1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS50076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGXG; 1.
DR Complete proteome.
SQ SEQUENCE 377 AA; 41078 MW; E66AA1F1606E775 CRC64;

Query Match 90.1%; Score 73; DB 16; Length 377;
Best Local Similarity 86.7%; Pred. No. 0.0003;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DQ |||||:|||||
60 QKRAAYDRFGHAAFE 74

RESULT 13
Q8FXX1 PRELIMINARY; PRT; 377 AA.
AC Q8FXX1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chaperone protein DnaJ.
GN DnaJ OR BR2126.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Unayam L., Brinkac L.M., Beanan M.U.,
RA Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.E.,
RA Redmiller S., Tetelehin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL: AE014500; AAN31016.1; -.
DR PIR: AC3502; AC3502.
DR TIGR: BR2126; -.
DR GO: GO:0003754; F:chaperone activity; IEA.
DR GO: GO:0003489; F:electron transporter activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR002939; DnaJ_C.
DR InterPro: IPR001305; DnaJ_CXXCXGXG.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR003095; Hsp_DnaJ.
DR Pfam: PF00226; DnaJ_1.
DR Pfam: PF01556; DnaJ_C; 1.
DR Pfam: PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS: PR00625; DnaJPROTEIN.
DR SMART: SM00271; DnaJ_1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS50076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGXG; 1.
DR Complete proteome.
SQ SEQUENCE 377 AA; 41078 MW; E66AA1F1606E775 CRC64;

Query Match 90.1%; Score 73; DB 16; Length 377;
```

```
Best Local Similarity 86.7%; Pred. No. 0.0003;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DQ |||||:|||||
60 QKRAAYDRFGHAAFE 74

RESULT 14
Q8RB67 PRELIMINARY; PRT; 384 AA.
AC Q8RB67;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Molecular chaperones (contain C-terminal Zn finger domain).
GN DnaJ OR TTE0956.
OS Thermanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermanaerobacteriales;
OC Thermanaerobacteriaceae; Thermanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=2192816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang U., Yu J., Yang H.,
RT "A complete sequence of T. tengcongensis genome."
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013061; AAM24212.1; -.
DR GO: GO:0003754; F:chaperone activity; IEA.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR002939; DnaJ_C.
DR InterPro: IPR001305; DnaJ_CXXCXGXG.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR003095; Hsp_DnaJ.
DR Pfam: PF00226; DnaJ_1.
DR Pfam: PF01556; DnaJ_C; 1.
DR Pfam: PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS: PR00625; DnaJPROTEIN.
DR SMART: SM00271; DnaJ_1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS50076; DnaJ_2; 1.
DR Complete proteome.
SQ SEQUENCE 384 AA; 42718 MW; 92B39791273F4094 CRC64;

Query Match 88.9%; Score 72; DB 16; Length 384;
Best Local Similarity 86.7%; Pred. No. 0.00046;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
DQ |||||:|||||
61 QKRAAYDRFGHAAFE 75

RESULT 15
Q7VOL3 PRELIMINARY; PRT; 377 AA.
AC Q7VOL3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DnaJ protein.
GN DnaJ OR BFL15.
OS Candidatus Blochmannia floridanus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
OX NCBI_TaxID=203907;
RN [1]
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RP SEQUENCE FROM N.A.
 RX MEDLINE=22784745; PubMed=12886019;
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
 RA Latorre A., Kausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
 RA van Ham R.C.H.J., Gross R., Moya A.;
 RT "The genome sequence of Blochmannia floridanus: comparative analysis
 of reduced genomes";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
 RL EMBL; BX248584; CADD3636.1; -.
 DR Complete proteome.
 KW SEQUENCE 377 AA; 41379 MM; 2047D0E868DB2A3E CRC64;
 SQ
 Query Match 86.4%; Score 70; DB 16; Length 377;
 Best Local Similarity 80.0%; Pred. NO. 0.00099;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QKRAAYDQYGHAF 15
 :||:|||||||
 Db 61 EKRSAYDQYGHAF 75

Search completed: August 17, 2004, 22:24:24
 Job time : 39 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 22:21:15 ; Search time 16 Seconds

(without alignments)
90.180 Million cell updates/sec

Title: US-09-616-247-4

Sequence: 1 GKRAADYGHAAFE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	376	1 HHECDJ	heat shock protein
2	81	100.0	376	2 G90630	DnaJ protein [limpo
3	81	100.0	376	2 G85481	chaperone with Dna
4	81	100.0	379	2 AB0058	chaperone protein
5	81	100.0	379	2 AF0503	DnaJ protein [limpo
6	81	100.0	394	2 G64112	heat shock protein
7	78	96.3	381	2 D82270	DnaJ protein VC085
8	77	95.1	392	2 S15295	nolC protein - Rhi
9	75	92.6	377	2 J05609	heat shock protein
10	75	92.6	377	2 F84947	DnaJ protein [limpo
11	73	90.1	373	2 D81242	DnaJ protein [limpo
12	73	90.1	375	2 B47042	heat shock protein
13	73	90.1	377	2 AC3502	chaperone protein
14	73	90.1	377	2 AD2591	molecular chaperon
15	73	90.1	377	2 D97373	chaperone protein
16	64	79.0	370	2 C71729	DnaJ protein [limpo
17	63	77.8	376	2 E70361	chaperone DnaJ - A
18	62	76.5	379	2 B35388	heat shock protein
19	62	76.5	377	2 A83052	DnaJ protein PA476
20	60	74.1	373	2 H97728	DnaJ protein [limpo
21	59	72.8	367	2 I40843	heat shock protein
22	58	71.6	379	2 A47079	heat shock protein
23	58	71.6	379	2 H86902	DnaJ protein [limpo
24	58	71.6	385	2 C87250	DnaJ protein [limpo
25	57	70.4	382	2 A49210	heat shock protein
26	57	70.4	364	2 D70164	heat shock protein
27	57	70.4	376	2 AD1621	heat shock protein
28	57	70.4	377	2 T43739	heat shock protein
29	57	70.4	377	2 AH1258	heat shock protein

ALIGNMENTS

RESULT 1
HHECDJ
heat shock protein dnaJ - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 01-Mar-2002
C:Accession: A92572; A26298; G40537; G64721; A26299
R:Barwell, J.C.A.; Tilly, K.; Craig, E.; King, J.; Zylitz, M.; Georgopoulos, C.
J. Biol. Chem. 261, 1782-1785, 1986
A:Title: The nucleotide sequence of the Escherichia coli K12 dnaJ gene.
A:Reference number: A92572; MUID:86111850; PMID:3003085
A:Accession: A92572
A:Molecule type: DNA
A:Residues: 1-376 <BAR>
A:Cross-references: GB:M12565; NID:g145767; PIDN:AAA23693.1; PID:g145769
A:Experimental source: strain K12
R:Ohki, M.; Tamura, F.; Nishimura, S.; Uchida, H.
J. Biol. Chem. 261, 1778-1781, 1986
A:Title: Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the
A:Reference number: A26298; MUID:86111849; PMID:3003084
A:Accession: A26298
A:Molecule type: DNA
A:Residues: 1-376 <OHK>
A:Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01990; G
R:Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizob
submitted to the EMBL Data Library, December 1992
A:Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-
A:Reference number: S40531
A:Accession: S40537
A:Molecule type: DNA
A:Residues: 1-376 <YUR>
A:Cross-references: EMBL:D10483; NID:g216434; PIDN:BA40192.1; PID:g216441
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G64721
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-376 <BLAT>
A:Cross-references: GB:AE00112; GB:U00096; NID:g1786192; PIDN:AACT3126.1; PID:g1786197,
C:Key words: DNA replication; heat shock; molecular chaperone; stress-induced protein
C:Comment: This protein is induced by heat shock under the control of the hcr gene proo
C:Genetics:
A:Gene: dnaJ
A:Map position: 0 min
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein
F:5-70/Domain: dnaJ amino-terminal homology <DNJ>
F:77-106/Region: G/F motif
F:144-151/Region: CXXCXGXG repeat
F:161-168/Region: CXXCXGXG repeat

F,183-190/Region: CXXCKXG repeat
F,197-204/Region: CXXCKXG repeat

Query Match 100.0%; Score 81; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKRAAYDQYGHAAFE 15
|||||

Db 61 OKRAAYDQYGHAAFE 75

RESULT 2

G90630 DnaJ protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C/Accession: G90630 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene

A/Reference number: A96629; MUID:21156231; PMID:11258796

A/Accession: G90630 A;Status: preliminary

A/Molecule type: DNA

A/Residues: 1-376 <HAV> A/Cross-references: GB:BA000007; PIDN:BA03438.1; PID:G13359471; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain RIMD 0509952

C/Genetics:

A/Gene: EC0015 C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

OY 1 OKRAAYDQYGHAAFE 15
|||||

Db 61 OKRAAYDQYGHAAFE 75

RESULT 3

G85481 chaperone with DnaJ, heat shock protein [imported] - Escherichia coli (strain O157:H7, S

C/Species: Escherichia coli C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C/Accession: G85481 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew

iller, U.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001 A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: AB5480; MUID:21074935; PMID:11206551

A/Accession: G85481 A;Status: preliminary

A/Molecule type: DNA A/Residues: 1-376 <STO> A/Cross-references: GB:AE005174; NID:G12512693; PIDN:AAG54315.1; GSPDB:GN00145; UWGP:Z00

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics: A/Gene: dnaJ C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKRAAYDQYGHAAFE 15
|||||

Db 61 OKRAAYDQYGHAAFE 75

RESULT 4

AB0058 chaperone protein DnaJ [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C/Accession: AB0058 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M.B.;

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.; E

ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E

Nature 413, 523-527, 2001 A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AB0058 A;Status: preliminary

A/Molecule type: DNA

A/Residues: 1-379 <KUR> A/Cross-references: GB:AL590842; PIDN:CAC89325.1; PID:G15978561; GSPDB:GN00175

C/Genetics:

A/Gene: dnaJ C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 81; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKRAAYDQYGHAAFE 15
|||||

Db 61 OKRAAYDQYGHAAFE 75

RESULT 5

AF0503 DnaJ protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)

C/Species: Salmonella enterica subsp. enterica serovar Typhi A/Note: this species has also been called Salmonella typhi

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AF0503 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerion, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AF0503 A;Status: preliminary

A/Molecule type: DNA

A/Residues: 1-379 <PAR> A/Cross-references: GB:AL513382; PIDN:CAD01166.1; PID:G16501296; GSPDB:GN00176

C/Genetics:

A/Gene: STY0013 C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

OY 1 OKRAAYDQYGHAAFE 15
|||||

Db 61 OKRAAYDQYGHAAFE 75

RESULT 6

CE4112 heat shock protein dnaJ - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Aug-1999

C/Accession: CE4112 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J

, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Georgagen, N.S.M. Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64112
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-394 <TIGR>
A:Cross-references: GB:L42023; GB:U32803; NID:g1574162; PINN:AAC22890.1; PID:g1574168; T
C:Genetics:
A:Gene: dnaJ
A:Start codon: GTG
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein
F:17-82/Domain: dnaJ amino-terminal homology <DNV>
F:89-121/Region: G/F motif
F:159-166/Region: CXXCXGXG repeat
F:176-183/Region: CXXCXGXG repeat
F:198-205/Region: CXXCXGXG repeat
F:212-219/Region: CXXCXGXG repeat

Query Match 100.0%; Score 81; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAF 15
DB 73 OKRAAYDQYGHAF 87

RESULT 7
D82270
dnaJ protein VC0856 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82270
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.J.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Drygiel, I.; Sellers, H.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82270
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-381 <HEI>
A:Cross-references: GB:AE004171; GB:AE003852; NID:96655308; PINN:AAF94018.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0856
A:Map position: 1
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 96.3%; Score 78; DB 2; Length 381;
Best Local Similarity 93.3%; Pred. No. 5.5e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAF 15
DB 61 OKRAAYDQYGHAF 75

RESULT 8
S15295
nolC protein - Rhizobium fredii
C:Species: Rhizobium fredii
C:Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 20-Aug-1999
C:Accession: S15295
R:Krishnan, H.B.; Pueppke, S.G.
Mol. Microbiol. 5, 737-745, 1991
A:Title: nolC, a Rhizobium fredii gene involved in cultivar-specific nodulation of soybean
A:Reference number: S15295; MUID:91260457; PMID:1646377
A:Accession: S15295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-392 <MOL>

A:Cross-references: GB:L03521; NID:g152353; PINN:AAA26333.1; PID:g152354
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F:4-69/Domain: dnaJ amino-terminal homology <DNV>

Query Match 95.1%; Score 77; DB 2; Length 392;
Best Local Similarity 93.3%; Pred. No. 8.4e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAF 15
DB 60 OKRAAYDQYGHAF 74

RESULT 9
JCS609
heat shock protein dnaJ - Buchnera sp.
C:Species: Buchnera sp.
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C:Accession: JCS609
R:Sato, S.; Ishikawa, H.
J. Biochem. 122, 41-48, 1997
A:Title: Structure and expression of the dnaJ operon of Buchnera, an intracellular sym
A:Reference number: JCS608; MUID:97420684; PMID:9276669
A:Accession: JCS609
A:Molecule type: DNA
A:Residues: 1-377 <SAT>
A:Cross-references: DDBJ:D88673; NID:g2351215; PINN:BAA21965.1; PID:g2351217
C:Comment: This protein binds to DnaK protein and GrpE protein and modulates the chaper
C:Genetics:
A:Gene: dnaJ
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C:Keywords: DNA replication; heat shock; molecular chaperone
F:5-70/Domain: dnaJ amino-terminal homology <DNV>
F:77-108/Region: G/F motif
F:145-152/Region: CXXCXGXG repeat
F:162-169/Region: CXXCXGXG repeat
F:184-191/Region: CXXCXGXG repeat
F:198-205/Region: CXXCXGXG repeat

Query Match 92.6%; Score 75; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 1.8e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAF 15
DB 61 EKRSAIDQYGHAF 75

RESULT 10
F84947
dnaJ protein [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: F84947
R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterium symbiont of aphids Buchnera sp.
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: F84947
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <STO>
A:Cross-references: GB:AF000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: dnaJ; B0152
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 92.6%; Score 75; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 1.8e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAF 15

DB 61 EKRAAYDQYGHAAFE 75

RESULT 11

DnaU protein NMA0209 [imported] - Neisseria meningitidis (strain MCS8 serogroup B, strain D81242
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C/Accession: D81242; C82015

R/RefSeq: H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathavan, V.; Gill, J.; Scariato, V.; Maignani, V.; Pizze, M. Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.

A/Reference number: A81000; MUID:20175755; PMID:10710307

A/Accession: D81242

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-373 <DET>

A/Cross-references: GB:AE002366; GB:AE002098; NID:97225284; PIDN:AAF40528.1; PID:9722528

A/Experimental source: serogroup B, strain MCS8

R/RefSeq: J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R/RefSeq: S.; Jørgensen, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A/Reference number: A81775; MUID:20225556; PMID:10761919

A/Accession: C82015

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-373 <PAR>

A/Cross-references: GB:AL162752; GB:AL157959; NID:97378778; PIDN:CAB83522.1; PID:9737897

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: dnaU; NMA0059; NMA0209

C/Superfamily: heat shock protein dnaU; dnaU amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 373;

Best Local Similarity 86.7%; Pred. No. 4.1e-05;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 61 EKRAAYDQYGHAAFE 75

RESULT 12

heat shock protein dnaU - Brucella ovis

C/Species: Brucella ovis
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999

C/Accession: B47042

R/RefSeq: M.F.; Teyssier, J.; Nicolas, M.; Liautaud, J.P.; Marti, J.; Sri Widadada, J. Bacteriol. 174, 8036-8042, 1992

A/Title: Cloning and characterization of the Brucella ovis heat shock protein DnaK func

A/Reference number: A47042; MUID:93094135; PMID:1459952

A/Accession: B47042

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-375 <CEI>

A/Cross-references: EMBL:M95799; NID:9144114; PIDN:MAC36133.1; PID:9144116

A/Note: sequence extracted from NCBI backbone (NCBIN:119966, NCBI:119968)

C/Genetics:

A/Gene: dnaU

C/Superfamily: heat shock protein dnaU; dnaU amino-terminal homology

C/Keywords: DNA replication; heat shock; molecular chaperone

F/4-69/Domain: dnaU amino-terminal homology <DN5>

F/76-108/Region: G/F motif

F/146-153/Region: CXXCXGXG repeat

F/163-170/Region: CXXCXGXG repeat

F/185-197/Region: CXXCXGXG repeat

F/199-206/Region: CXXCXGXG repeat

F/199-206/Region: CXXCXGXG repeat

Query Match 90.1%; Score 73; DB 2; Length 375;
Best Local Similarity 86.7%; Pred. No. 4.1e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 60 QKRAAYDRFGHAAFE 74

RESULT 13

chaperone protein dnaU [imported] - Brucella melitensis (strain 16M)

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C/Accession: AC3502

R/RefSeq: H.; Goldstein, V.G.; Kaput, V.; Redkar, R.U.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I. Mazur, M.; Goldstein, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesec Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688

A/Accession: AC3502

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-377 <KUR>

A/Cross-references: GB:AE008917; PIDN:ALU53182.1; PID:97984054; GSPDB:GN00190

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BMEI2001

A/Map position: 1

C/Superfamily: heat shock protein dnaU; dnaU amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 377;

Best Local Similarity 86.7%; Pred. No. 4.1e-05;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 60 QKRAAYDRFGHAAFE 74

RESULT 14

molecular chaperone, DnaU family dnaU [imported] - Agrobacterium tumefaciens (strain C58

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C/Accession: AD2591

R/RefSeq: D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AD2591

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-377 <KUR>

A/Cross-references: GB:AE006888; PIDN:AAU1146.1; PID:917738442; GSPDB:GN00186

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Gene: dnaU

A/Map position: circular chromosome

C/Superfamily: heat shock protein dnaU; dnaU amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 377;

Best Local Similarity 86.7%; Pred. No. 4.1e-05;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

DB 61 QKRAAYDRFGHAAFE 75

RESULT 15

D97373
 chaperone protein dnaJ [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: D97373
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: D97373
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-377 <KOR>
 A:Cross-references: GB:AE07869; PIDN:AAK9541.1; PID:G15154994; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_192
 A:Map position: circular chromosome
 C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 90.1%; Score 73; DB 2; Length 377;
 Best Local Similarity 86.7%; Pred. No. 4.1e-05;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQXGHAF 15
 |||||:|||||
 Db 61 OKRAAYDRFGHAF 75

Search completed: August 17, 2004, 22:24:49
 Job time : 16 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 22:13:09 ; Search time 52 Seconds
(without alignments)
81,504 Million cell updates/sec

Title: US-09-616-247-4
Perfect score: 81
Sequence: 1 QKRAAYDQYGHAAFE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	15	AAW25795	AAW25795 Peptide d
2	81	100.0	15	AAW79543	AAW79543 E. coli d
3	81	100.0	15	AAW99341	AAW99341 Vaccine r
4	81	100.0	15	AAU09842	AAU09842 E. coli dn
5	81	100.0	15	AAU98876	AAU98876 E. coli d
6	81	100.0	15	AAE19457	AAE19457 Human hea
7	81	100.0	15	ABR55132	ABR55132 E. coli d
8	81	100.0	16	AAW99344	AAW99344 Vaccine r
9	81	100.0	16	AAU98852	AAU98852 E. coli DN
10	81	100.0	16	ABR55126	ABR55126 E. coli d
11	81	100.0	118	AAU02075	AAU02075 Synthetic
12	81	100.0	131	AAAB11396	AAAB11396 E. coli e
13	81	100.0	131	AAAB74197	AAAB74197 OmpA-U do
14	81	100.0	131	AAAB70767	AAAB70767 Expressio
15	81	100.0	131	AAW72018	AAW72018 E. coli O
16	81	100.0	340	AAU17588	AAU17588 Novel sig
17	81	100.0	340	ADB94296	ADB94296 Human nov
18	81	100.0	341	AAU17587	AAU17587 Novel sig
19	81	100.0	341	ADB84295	ADB84295 Human nov
20	81	100.0	373	ABM67485	ABM67485 Human nov
21	81	100.0	399	AAAB11395	AAAB11395 E. coli e
22	81	100.0	399	AAAB74196	AAAB74196 OmpA-Dnat
23	81	100.0	399	AAAB70766	AAAB70766 Expressio
24	81	100.0	399	AAW72017	AAW72017 E. coli O
25	81	100.0	459	AAU02077	AAU02077 Synthetic

26	81	100.0	476	4	ABG17771
27	73	90.1	344	6	ABP80877
28	72	88.9	15	2	AAW95446
29	72	88.9	15	2	AAW25796
30	72	88.9	15	2	AAE19458
31	72	88.9	15	6	ABR55133
32	64.5	79.6	14	2	AAW95445
33	61	75.3	385	6	ABD10662
34	58	71.6	332	3	AAW14804
35	58	71.6	367	3	AAW14803
36	58	71.6	379	5	ABW5579
37	58	71.6	456	3	AAW14802
38	57	70.4	377	5	ABW48799
39	56	69.1	352	2	AAW22358
40	56	69.1	378	6	ABU00882
41	56	69.1	378	6	ABP81556
42	56	69.1	379	5	ABP28852
43	56	69.1	396	5	ABP28853
44	55	67.9	368	3	AAW05934
45	54	66.7	15	2	AAW25798

ALIGNMENTS

RESULT 1
AAW25795
ID AAW25795 standard; peptide: 15 AA.

AC AAW25795;
XX 06-APR-1998 (first entry)

DE Peptide dnaup1 which protects against arthritogenic peptides.

CC HLA or in populations of *E. coli* in the gastrointestinal tract
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.8e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
 |||||
 Db 1 OKRAAYDQYGHAAFE 15

RESULT 2
 AAY79543
 ID AAY79543 standard; peptide; 15 AA.
 XX

AC AAY79543;
 XX
 DT 15-AUG-2000 (first entry)
 XX

DE *E. coli* dnaJp1 heat shock protein peptide.

KW Antigen presenting cell; T-lymphocyte; T-cell; immunomodulator;
 KW autoimmune disease; allergy; cancer; infection; graft rejection;
 KW immunotherapy; therapy; major histocompatibility complex; MHC; dnaJp1;
 KW heat shock protein.

XX *Escherichia coli*.

OS
 XX WO200023053-A2.

XX 27-APR-2000.

XX 19-OCT-1999; 99WO-US024666.

XX 20-OCT-1998; 98US-0105018P.

XX (ALBA/) ALBANI S.

XX ALBANI S;

XX WPI; 2000-339492/29.

PT New artificial antigen presenting cells useful for isolating and
 PT expanding T cells, and modulating T cell responses for the treatment of
 PT e.g. autoimmune diseases, allergies.

XX Disclosure; Page 42; 179pp; English.

XX This peptide is derived from *Escherichia coli* heat shock protein dnaJp1.
 CC Novel artificial antigen presenting cells (APC) of the invention comprise
 CC antigens, such as the present peptide, that are presented by a major
 CC histocompatibility complex (MHC) component for contact with, and
 CC recognition by, a T cell receptor. The invention is directed to
 CC artificial APC and methods of making APC, which are used to isolate and
 CC expand T cell populations and to modulate T cell responses. The invention
 CC also provides novel methods for the identification and isolation and
 CC antigen-specific T cells. The methods provide for the construction of
 CC liposomes containing MHC:peptide complexes, accessory molecules, co-
 CC stimulatory molecules, adhesion molecules, and other molecules irrelevant
 CC to T cell binding or modulation that are used in the binding of
 CC artificial APC to solid support systems that may be used in the retrieval
 CC and identification and antigen-specific T cells. Devices and methods are
 CC provided for treating conditions that would benefit from modulation of T
 CC cell response, e.g. autoimmune disorders (especially type I diabetes
 CC mellitus, multiple sclerosis, rheumatoid arthritis, dermatomyositis,
 CC juvenile rheumatoid arthritis and uveitis), allergies, cancer, viral
 CC infections, and graft rejection

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.8e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
 |||||
 Db 1 OKRAAYDQYGHAAFE 15

RESULT 3
 AAM9341
 ID AAM9341 standard; peptide; 15 AA.
 XX

AC AAM9341;

XX 07-DEC-2001 (first entry)

DE Vaccine related MHC ligand peptide SEQ ID NO:444.

XX Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
 KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
 KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
 KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
 KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
 KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
 KW human immunodeficiency virus.

XX Homo sapiens.

XX WO200170772-A2.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-FR000872.

XX 23-MAR-2000; 2000FR-00003711.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Klingner-Hamouir C, Corvaia N, Beck A, Goetsch L;

XX WPI; 2001-611470/70.

PT Stabilized pharmaceutical containing N-terminal glutamic acid or
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 PT with strong acid.

XX Claim 9; Page 107; 149pp; French.

XX The present invention describes a pharmaceutical compound (I) that
 CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
 CC the form of an addition salt with a strong, physiologically acceptable
 CC acid (II). Also described are: (a) a pharmaceutical composition
 CC containing at least one (I); (b) a vaccine containing at least one (I)
 CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
 CC method for in vitro diagnosis of diseases associated with the presence of
 CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
 CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
 CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
 CC cytostatic activities. (I) are useful, in human or veterinary medicine,
 CC in pharmaceutical compositions (for treating immune disorders, e.g.
 CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
 CC rejection, infection, hormonal disorders and central nervous system
 CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
 CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
 CC infections; or (ii) of cancers. A particular application is in anti-
 CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
 CC associated with interactions between MHC and (I), e.g. melanoma and human
 CC immunodeficiency virus infection. AAM9341 to AAM9342 represent peptides
 CC which can be used in pharmaceutical compounds from the present invention

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
DB 1 OKRAAYDQYGHAAFE 15

RESULT 4
ID AAU09842 standard; peptide; 15 AA.
AC AAU09842;
XX
XX 26-FEB-2002 (first entry)
DE E.coli dnaup1 heat shock protein-derived peptide.
XX
XX Antigenic; antidiabetic; neuroprotective; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; ophthalmological; anti-allergic;
KW cytostatic; virucide; antibacterial; artificial antigen presenting cell;
KW liposome; major histocompatibility complex; MHC; T cell; allograft;
KW cytokine production; T-helper 2 response; transplantation therapy;
KW autoimmune disease; type 1 diabetes mellitus; multiple sclerosis;
KW rheumatoid arthritis; dermatomyositis; juvenile rheumatoid arthritis;
KW uveitis; allergy; cancer; infection; dnaup1 heat shock protein.
XX
XX Escherichia coli.
OS
XX WO200180833-A1.
PN
XX 01-NOV-2001.
PD
XX 20-APR-2000; 2000WO-IT000161.
PE
XX 20-APR-2000; 2000WO-IT000161.
PR
XX 20-APR-2000; 2000WO-IT000161.
XX
XX (ALBA/) ALBANI S.
PA
XX
XX Albani S;
PI
XX WPI; 2002-055316/07.
DR
XX
XX New artificial antigen presenting cell, useful for modulating T cell
PT response for treating allergies and cancers, comprises liposome, major
PT histocompatibility complex, antigen and accessory molecule components.
XX
XX Disclosure; Page 46; 195pp; English.

The invention relates to an artificial antigen presenting cell (1) comprising liposome, major histocompatibility complex (MHC), antigen and accessory molecule components. (1) is used in methods for the following: (1) identifying T cells specific for an antigen of interest; (2) isolating T cells specific for an antigen of interest; (3) modulating T cell response; (4) characterising the functional state of antigen-specific T cells; (5) treating a condition in a subject which would be benefited by altering the functional pattern of cytokine production by certain antigen-specific T cells to increase T-helper (Th) 2 response and/or decrease Th1 response; (6) identifying antigen-specific T cells specific for epitopes on a graft donor's tissue likely to elicit graft versus host rejection response; and (7) treating a recipient mammal to reduce rejection of allografts in a transplantation therapy regime.

Method (5) is useful for treating autoimmune disease such as type 1 diabetes mellitus, multiple sclerosis, rheumatoid arthritis, dermatomyositis, juvenile rheumatoid arthritis or uveitis. Alternatively it is useful for treating allergy due to allergens such as dust, animal skin bypass products, vegetables, fruits, pollen or chemicals, cancer, viral infection, bacterial infection. Addition of the accessory molecules, as well as co-stimulatory molecules, and other proteins in proper orientation in the liposomes allow for substantially improved binding association and manipulation of T cells which is very important in the identification and stimulation of antigen-specific T cells. The present sequence represents E.coli dnaup1 heat shock protein-derived

CC peptide used in the method of the invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
DB 1 OKRAAYDQYGHAAFE 15

RESULT 5
ID AAU98876 standard; peptide; 15 AA.
AC AAU98876;
XX
XX 22-AUG-2002 (first entry)
DE E. coli DNAB PI immunogenic peptide.
XX
XX Immunogenic peptide; heat shock protein; HSP; DNAB; immunomodulatory;
KW cytosolic; anti-inflammatory; antibacterial; antiarthritic; human;
KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
KW infectious disease; inflammatory bowel disease; cancer; HDU2;
KW mucosal tolerisation; DNA vaccination; energy induction.
XX
XX Escherichia coli.
OS
XX WO200236611-A2.
PN
XX 10-MAY-2002.
PD
XX 31-OCT-2001; 2001WO-US045344.
PE
XX 01-NOV-2000; 2000US-0245181P.
PR
XX (REGC) UNIV CALIFORNIA.
PA (MART) MARTINI A.
XX
XX Martini A, Albani S, Carson DA, Praxen BJ;
PI
XX WPI; 2002-48999/52.
DR
XX

New immunomodulatory peptides from heat shock proteins, useful for treating immunological disorder in subjects such as humans, e.g. autoimmune disease (e.g. arthritis), infectious disease, inflammatory bowel disease or cancer.

Example 8; Page 53; 84pp; English.

This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnf heat shock protein (hsp) in modulating an immune response in a subject. The peptides of the invention may have immunomodulatory, cytostatic, anti-inflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The immunogenic peptide is useful for modulating (i.e. augmenting/inducing or reducing/inhibiting) an immune response in a subject having an immunological disorder (e.g. autoimmune disease such as arthritis or articular juvenile idiopathic arthritis), an infectious disease or inflammatory bowel disease or cancer. The immunogenic peptide of the invention is also useful for modulating immunoeffect or cell responsiveness in a subject. The immunogenic peptide is particularly useful for treating the above-mentioned diseases in mammals, e.g. cat, dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In general, the peptide is useful in methods involving mucosal tolerisation, DNA vaccination, energy induction or active immunisation. The present sequence represents the E.coli DNAB PI immunogenic peptide of the invention

SQ Sequence 15 AA; Query Match 100.0%; Score 81; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.8e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 Db 1 QKRAAYDQYGHAAFE 15

RESULT 6
 ID AAE19457 standard; peptide; 15 AA.
 XX AAE19457;
 AC AAE19457;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Human heat shock protein (hsp) dnaup1 peptide.
 XX
 KW Human; human leukocyte antigen; HLA; DR-binding peptide; therapy;
 KW stress protein; major histocompatibility complex; MHC; antiulcer;
 KW type I diabetes; scleroderma; heat shock protein; hsp; vitiligo;
 KW rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour;
 KW ulcerative colitis; infectious disease; haemostatic; nephrotropic;
 KW polymyositis; chronic active hepatitis; primary biliary cirrhosis;
 KW pernicious anaemia; autoimmune thyroiditis; Sjogren's syndrome; cancer;
 KW Grave's disease; autoimmune disease; multiple sclerosis; hepatotropic;
 KW inflammatory bowel disease; Goodpasture's syndrome; neuoprotective;
 KW antimicrobial; immunosuppressive; dermatological; antiinflammatory;
 KW antifertility; idiopathic Addison's disease; cytostatic.
 KW
 XX Homo sapiens.
 OS
 XX WO200212286-A2.
 EN 14-FEB-2002.
 PD
 XX 08-AUG-2001; 2001WO-US041656.
 PE
 XX 09-AUG-2000; 2000US-0224104P.
 PR 06-APR-2001; 2001US-00828574.
 XX
 PA (UYCA-) UNIV CALIFORNIA SAN DIEGO.
 XX
 PI Albani S, Prakken BJ;
 DR WPI: 2002-227137/28.
 XX
 PT Novel human leukocyte antigen pan DR-binding peptide, useful for treating
 PT immune mediated diseases and conditions, has a fragment of stress protein
 PT that binds to major histocompatibility complex class II molecules.
 PS Claim 9; Page 45; 68pp; English.

The invention relates to human leukocyte antigen (HLA) pan DR-binding
 peptide comprising a fragment of a stress protein that binds to one or
 more major histocompatibility complex (MHC) class II molecules. The
 invention also relates to heat shock protein (hsp) peptides. The peptides
 of the invention and the immunomodulating composition comprising these
 peptides are useful for modulating, treating or preventing an immune-
 mediated disease in a mammalian subject e.g. human, having or at risk of
 having a disease including autoimmune disease, multiple sclerosis (MS),
 rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I
 diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma,
 lymphoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours,
 retinoblastoma, sarcoma and connective tissue cancers) and infectious
 diseases. The peptides of the invention are also useful for screening
 peptides or analogues that modulate pathogenic immune response. These
 peptides are useful for treating autoimmune diseases or disorders
 including Sjogren's syndrome, polymyositis, chronic active hepatitis,
 mixed connective tissue disease, primary biliary cirrhosis, pernicious

CC anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease,
 CC gluten-sensitive enteropathy, Grave's disease, inflammatory bowel
 CC disease, autoimmune neutropenia, idiopathic thrombocytopenia purpura,
 CC pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome,
 CC bullous pemphigoid, discoid lupus and dense deposit disease. The present
 CC sequence is human hsp dnaup1 peptide used in the exemplification of the
 CC invention

SQ Sequence 15 AA; Query Match 100.0%; Score 81; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.8e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 Db 1 QKRAAYDQYGHAAFE 15

RESULT 7
 ID ABR55132 standard; peptide; 15 AA.
 XX ABR55132;
 AC ABR55132;
 XX
 DT 03-JUL-2003 (first entry)
 XX
 DE E. coli Dnaup1 antigen-specific epitope peptide.
 XX
 KW Antigen-specific epitope; immune response; T cell; cytokine;
 KW antidiabetic; antidiabetic; neuroprotective; anti-inflammatory;
 KW cytosaric; antihypoid; anti-asthmatic; immunosuppressive;
 KW antiporiatic; anti-ulcer; antianaemic; cardiant; respiratory;
 KW antiallergic; dermatological; antiporiatic.
 KW
 XX Escherichia coli.
 OS
 XX WO2003026579-A2.
 EN 03-APR-2003.
 PD
 XX 25-SEP-2002; 2002WO-US030578.
 PE
 XX 25-SEP-2001; 2001US-0325499P.
 PR 11-DEC-2001; 2001US-0339284P.
 XX
 PA (REBC) UNIV CALIFORNIA.
 XX
 PI Albani S, Martins A;
 DR WPI: 2003-430097/40.
 XX
 PT Modulating an immune response in a subject having an immune-related
 PT disorder, e.g. arthritis by administering an antigen-specific epitope and
 PT a cytokine or an agent that effects cytokine activity or expression.
 PS Disclosure; Page 9; 41pp; English.

The invention relates to a novel method for modulating an immune response
 in a subject having an immune-related disorder. The method comprises: (a)
 administering an antigen-specific epitope, where administration provides
 CC epitope-specific T cell immune modulation; and (b) administering a
 CC cytokine, an agent that effects cytokine activity or expression, or an
 CC anticytokine therapy. The method of the invention has antiarthritic,
 CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
 CC antihypoid, anti-asthmatic, immunosuppressive, antiporiatic, anti-
 CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
 CC dermatological, and antiporiatic activity. The method is useful for
 CC modulating an immune response in a subject having an immune-related
 CC disorder. The present sequence is used in the exemplification of the
 CC invention

SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.8e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 |||||
 DB 1 QKRAAYDQYGHAAFE 15

RESULT 8

AAM99344
 ID AAM99344 standard; peptide; 16 AA.

AC AAM99344;

DT 07-DEC-2001 (first entry)

DE Vaccine related MHC ligand peptide SEQ ID NO:447.

KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
 KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
 KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
 KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
 KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
 KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
 KW human immunodeficiency virus.

OS Homo sapiens.

PN WO200170772-A2.

PD 27-SEP-2001.

PF 22-MAR-2001; 2001WO-FR000872.

PR 23-MAR-2000; 2000FR-00003711.

PA (FABR) FABRE MEDICAMENT SA PIERRE.

PI Klingner-Hamour C, Corvaia N, Beck A, Goetsch L;

DR WPI: 2001-611470/70.

PT Stabilized pharmaceutical containing N-terminal glutamic acid or
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 PT with strong acid.

PS Claim 9; Page 107; 149pp; French.

CC The present invention describes a pharmaceutical compound (I) that
 CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
 CC the form of an addition salt with a strong, physiologically acceptable
 CC acid (II). Also described are: (a) a pharmaceutical composition
 CC containing at least one (I); (b) a vaccine containing at least one (I)
 CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
 CC method for in vitro diagnosis of diseases associated with the presence of
 CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
 CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
 CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal, and
 CC cytostatic activities. (I) are useful, in human or veterinary medicine,
 CC in pharmaceutical compositions (for treating immune disorders, e.g.
 CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
 CC rejection, infection, hormonal disorders and central nervous system
 CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
 CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
 CC infections; or (ii) of cancers. A particular application is in anti-
 CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
 CC associated with interactions between MHC and (I), e.g. melanoma and human
 CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
 CC which can be used in pharmaceutical compounds from the present invention
 CC
 CC Sequence 16 AA;

Query Match 100.0%; Score 81; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
 |||||
 DB 1 QKRAAYDQYGHAAFE 15

RESULT 9

AU98852
 ID AU98852 standard; peptide; 16 AA.

AC AU98852;

DT 22-AUG-2002 (first entry)

DE E.Coli DNA 61 immunogenic peptide.

KW Immunogenic peptide; heat shock protein; HSP; DNA; immunomodulatory;
 KW cytostatic; antiinflammatory; antibacterial; antiarthritic;
 KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
 KW infectious disease; inflammatory bowel disease; cancer;
 KW mucosal tolerisation; DNA vaccination; energy induction.

OS Escherichia coli.

PN WO200236611-A2.

PD 10-MAY-2002.

PF 31-OCT-2001; 2001WO-US045344.

PR 01-NOV-2000; 2000US-0245181P.

PA (REGC) UNIV CALIFORNIA.

PA (MART/) MARTINI A.

PI Martini A, Albani S, Carson DA, Frakken BJ;

DR WPI: 2002-489999/52.

PT New immunomodulatory peptides from heat shock proteins, useful for
 PT treating immunological disorder in subjects such as humans, e.g.
 PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory
 PT bowel disease or cancer.

PS Claim 4; Page 55; 84pp; English.

CC This invention relates to the use of a peptide, which is an immunogenic
 CC portion derived from a draft heat shock protein (hsp) in modulating an
 CC immune response in a subject. The peptides of the invention may have
 CC immunomodulatory, cytostatic, antiinflammatory, antibacterial or
 CC antiallergic properties and can stimulate expression of interleukins,
 CC tumour necrosis factor and transforming growth factor beta. The
 CC immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
 CC reducing/inhibiting) an immune response in a subject having an
 CC immunological disorder (e.g. autoimmune disease such as arthritis or
 CC articular juvenile idiopathic arthritis), an infectious disease, an
 CC inflammatory bowel disease or cancer. The immunogenic peptide of the
 CC invention is also useful for modulating immunoeffector cell
 CC responsiveness in a subject. The immunogenic peptide is particularly
 CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
 CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
 CC general, the peptide is useful in methods involving mucosal tolerisation,
 CC DNA vaccination, energy induction or active immunisation. The present
 CC sequence represents an E. coli DNA immunogenic peptide of the invention
 CC
 CC Sequence 16 AA;

Query Match 100.0%; Score 81; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;


```

XX      Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by
PT simultaneous expression of a chaperone protein, allows simple recovery
PT from periplasm or medium.
XX
XX      Disclosure; Page 15; 36pp; German.
PS
CC      This invention describes a novel method for preparing a naturally folded
CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged
CC Cys residues by culturing prokaryotic cells that contain an expression
CC vector for (I) including a prokaryotic signal sequence at its N-terminus
CC and a nucleic acid (II) that secretes a chaperone protein (III) into the
CC periplasm. (I) is secreted into the periplasm or medium; the signal
CC peptide is then cleaved and (I) isolated from the periplasm or medium.
CC The method is used for production of antibody, interferon, protein
CC hormone or protease. Expression of (III) increases the yield of (I). The
CC method is simple and eliminates time-consuming in vitro processing
CC operations such as dissolution of inclusion bodies, reduction and
CC refolding. (III) protects (I) against agglomeration and promotes their
CC natural conformation
CC
SQ      Sequence 131 AA;
XX
XX      Query Match          100.0%; Score 81; DB 4; Length 131;
XX      Best Local Similarity 100.0%; Pred. No. 1.1e-06;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY      1 QKRAAYDQYGHAAFE 15
XX      |||||
DB      84 QKRAAYDQYGHAAFE 98
XX
XX      RESULT 15
XX      ID AAY72018 standard; protein; 131 AA.
XX      AC AAY72018;
XX      DT 28-MAR-2001 (first entry)
XX      DE E. coli OmpA-J domain fusion protein encoded by pUBS520-pJN-J-domain.
XX      KM Secreted protein; chaperone; interferon; protease; hormone;
XX      KW fusion protein; naturally folded protein; lac-1pp promoter; DnaJ,
XX      OS heat shock protein; HSP; outer membrane protein A; OmpA; J domain.
XX      ES Escherichia coli.
XX      EP EP1054063-A2.
XX      FN
XX      PD 22-NOV-2000.
XX      PF 19-APR-2000; 2000EP-00108505.
XX      PR 26-APR-1993; 99EP-00107412.
XX      PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
XX      DR MPI: 2001-03377/05.
XX      N-PSDB; AAD02210.
XX
XX      Producing water-soluble, naturally folded, and secreted eukaryotic
PT polypeptide, involves culturing prokaryotic cells containing an
PT expression vector encoding the polypeptide in the presence of arginine or
PT a specific compound.
XX
XX      Example 3; Page 17; 35pp; English.
XX
XX      The patent discloses a method for the production of a water-soluble,
CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.
CC The method involves culturing the prokaryotic cells, containing an

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CC expression vector encoding the desired protein and the prokaryotic signal
CC sequence, in the presence of an additive, e.g., L-arginine. The signal
CC sequence mediates the secretion of the desired protein into the
CC periplasm, where folding of the protein takes place. The prokaryotic cell
CC also contains an expression vector encoding a molecular chaperone, e.g.,
CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-
CC overexpression and co-secretion of molecular chaperones in the periplasm
CC improves the yield of functionally folded protein. The above method
CC recombinantly produces a high yield of eukaryotic secreted proteins in
CC prokaryotes. The method is useful for producing eukaryotic proteins such
CC as an antibody, antibody fragment, interferon, colony hormone or a
CC protease. The present sequence is an Escherichia coli outer membrane
CC protein A (OmpA) signal sequence-J domain fusion protein encoded by
CC pUBS520-p1N-J-domain. The plasmid, pUBS520-p1N-J-domain, also contains
CC the lac-p1 promoter and the lpp terminator. The periplasmic co-secretion
CC of J domain, which is the N-terminal portion of the DnaJ, facilitates the
CC folding of the desired secreted protein

XX Sequence 131 AA;

Query Match 100.0%; Score 81; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 1,1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDYGHAFF 15
|||||
DB 84 OKRAAYDYGHAFF 98

Search completed: August 17, 2004, 22:23:11
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 22:13:49 ; Search time 13 Seconds

(without alignments)
60.081 Million cell updates/sec

Title: US-09-616-247-4
Perfect score: 81
Sequence: 1 QKRAAYQYGHAAFE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	375	1 DNAJ_ECOLI	P08622 escherichia
2	81	100.0	377	1 DNAJ_HAEDU	P48208 haemophilus
3	81	100.0	378	1 DNAJ_SALTY	O60004 salmonella
4	81	100.0	382	1 DNAJ_HARIN	P43735 haemophilus
5	78	96.3	375	1 DNAJ_ACTAC	P77866 actinobacil
6	78	96.3	381	1 DNAJ_VIBCH	O34242 vibrio chol
7	78	96.3	385	1 DNAJ_VIBHA	O87385 vibrio harv
8	77	95.1	234	1 DNAJ_RHILB	O33529 rhizobium 1
9	77	95.1	392	1 NOLC_RHIFR	P26508 rhizobium 2
10	75	92.6	372	1 DNAJ_PASMU	Q92682 pasteurella
11	75	92.6	377	1 DNAJ_BUCAI	O32465 buchiera ap
12	74	90.1	378	1 DNAJ_BUCAP	O8k9y9 buchiera ap
13	73	90.1	373	1 DNAJ_NEIMA	P57107 neisseria m
14	73	90.1	375	1 DNAJ_BRIOV	O00980 brucella ov
15	73	90.1	377	1 DNAJ_AGR75	P50018 agrobacteri
16	73	90.1	377	1 DNAJ_BRUME	O8ey77 brucella me
17	73	90.1	377	1 DNAJ_BROSE	O8ifx1 brucella su
18	72	88.9	379	1 DNAJ_RHOSP	O08386 rhodopseudo
19	70	86.4	379	1 DNAJ_PASHA	O52065 pasteurella
20	70	86.4	383	1 DNAJ_BUCBP	O89au7 buchiera ap
21	69	85.2	384	1 DNAJ_RHOCA	O52702 rhodobacter
22	68	84.0	370	1 DNAJ_ERRRH	O05646 erysipeloth
23	68	84.0	377	1 DNAJ_BRJVA	P94319 bradyrhizob
24	67	82.7	371	1 DNAJ_METSS	O92fcs methylovoru
25	66	81.5	383	1 DNAJ_LACSK	O87778 lactobacill
26	64	79.0	370	1 DNAJ_RICPR	O92dy0 rickettsia
27	63	77.8	376	1 DNAJ_AQIAE	O66921 aquifex aeo
28	63	77.8	379	1 DNAJ_LEGPN	P50025 legionella
29	62	76.5	377	1 DNAJ_PSEAE	Q9hva4 pseudomonas
30	59	72.8	374	1 DNAJ_COXBU	P42381 coxiella bu
31	58	71.6	379	1 DNAJ_LACLA	P35514 lactococcus
32	58	71.6	385	1 DNAJ_CAUCR	P22305 caulobacter
33	57	70.4	364	1 DNAJ_BORBU	P28616 borrelia bu

34	57	70.4	369	1 DNAJ_NITEU	O06431 nitrosomona
35	57	70.4	376	1 DNAJ_LISIN	O92bng listeria in
36	57	70.4	377	1 DNAJ_LISMO	O955a3 listeria mo
37	56	69.1	368	1 DNAJ_XYLEPA	Q9p006 xyella fas
38	56	69.1	368	1 DNAJ_XYLEP	O87bs9 xyella fas
39	56	69.1	378	1 DNAJ_STRPN	P95830 streptococc
40	54	66.7	383	1 DNAJ_FORGI	O9xca6 porphyromon
41	53	65.4	307	1 DNAJ_DEIPR	O34136 deinococcus
42	52	64.2	372	1 DNAJ_BACSU	P17631 bacillus su
43	52	64.2	376	1 DNAJ_METTH	O27352 methanobact
44	52	64.2	389	1 DNAJ_METVA	P35515 methanosarc
45	50	61.7	368	1 DNAJ_BACSH	O69269 bacillus sp

ALIGNMENTS

RESULT 1
ID DNAJ_ECOLI STANDARD; PRT; 375 AA.
AC P08622;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaJ (Heat shock protein J) (HSP40).
GN DNAJ OR GRP OR B0015.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RX MEDLINE=6111849; PubMed=3003085.
RA Ohki M., Tamura F., Nishimura S., Uchida H.;
RT "Nucleotide sequence of the Escherichia coli dnaJ gene and
RT purification of the gene product.";
RL J. Biol. Chem. 261:1778-1781(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RA MEDLINE=8111850; PubMed=3003085.
RA Bardwell J.C.A., Tilly K., Craig E., King J., Zylitz M.,
RA Georgopoulos C.;
RT "The nucleotide sequence of the Escherichia coli K12 dnaJ+ gene. A
RT gene that encodes a heat shock protein.";
RL J. Biol. Chem. 261:1782-1785(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RA MEDLINE=92334977; PubMed=1630901;
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA Isono K., Mizobuchi K., Nakata A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RT the 0-2.4 min region.";
RL Nucleic Acids Res. 20:3305-3308(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G., III, Bloch C.A., Ferna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:12453-12474(1997).
RN [5]
RP POSSIBLE FUNCTION.
RX MEDLINE=91187894; PubMed=1826368;
RA Liberek K., Marszałek J., Ang D., Georgopoulos C., Zylitz M.;
RT "Escherichia coli DnaJ and GrpJ heat shock proteins jointly stimulate
RT ATPase activity of DnaK.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878(1991).
RN [6]

RP STRUCTURE BY NMR OF 1-107.
 RX MEDLINE=96291434; PubMed=8764403;
 RA Pellechia M., Szyperiski T., Wall D., Georgopoulos C., Wuehrich K.;
 RT "NMR structure of the J-domain and the Gly/Phe-rich region of the
 RT Escherichia coli DnaJ chaperone.";
 RL J. Mol. Biol. 260:236-250(1996).
 RN [7]
 RP STRUCTURE BY NMR OF 1-104.
 RX MEDLINE=99224904; PubMed=10210198;
 RA Huang K., Flanagan J.M., Prestegard J.H.;
 RT "The influence of C-terminal extension on the structure of the 'J-
 RT domain' in E. coli DnaJ.";
 RL Protein Sci. 8:203-214(1999).
 RN [8]
 RP STRUCTURE BY NMR OF 130-208.
 RX MEDLINE=20351465; PubMed=10891270;
 RA Martinez-Yamout M., Legge G.B., Zhang O., Wright P.E., Dyson H.J.;
 RT "Solution structure of the cysteine-rich domain of the Escherichia
 RT coli chaperone protein DnaJ.";
 RL J. Mol. Biol. 300:805-818(2000).
 CC -1- FUNCTION: INTERACTS WITH DNA, TO DISASSEMBLE A PROTEIN COMPLEX
 CC AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY
 CC WITH GRPE, THE ATPASE ACTIVITY OF DNAK.
 CC -1- COFACTOR: Binds 2 zinc ions per monomer.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- INDUCTION: BY HEAT SHOCK UNDER THE CONTROL OF THE HTRP REGULATORY
 CC PROTEIN.
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -----
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 CC -----
 DR EMBL; M12565; AAA23693.1; -;
 DR EMBL; D10483; BAB96590.1; -;
 DR EMBL; AE000112; AAC73126.1; -;
 DR PIR; A92572; HHRCDB.
 DR PDB; 1XBL; 11-JAN-97.
 DR PDB; 1BOQ; 15-JUN-99.
 DR PDB; 1BOZ; 15-JUN-99.
 DR PDB; 1EXK; 26-JUL-00.
 DR EC02DBASE; H036.5; 6TH EDITION.
 DR EcoGene; EG10240; dnaJ.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXKXGKXG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40 DnaJ_dep.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXKXGKXG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SMO0271; DnaJ_1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS50076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXKXGKXG; 1.
 DR Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
 KW 3D-structure; Complete proteome.
 FT INIT MET 0
 FT DOMAIN 2 71 J-DOMAIN.
 FT DOMAIN 76 113 GY-RICH.
 FT REPEAT 143 150 CXKXGKXG MOTIF.
 FT REPEAT 160 167 CXKXGKXG MOTIF.
 FT REPEAT 182 189 CXKXGKXG MOTIF.
 FT REPEAT 196 203 CXKXGKXG MOTIF.
 FT METAL 143 143 ZINC 1.

FT METAL 146 146 ZINC 1.
 FT METAL 160 160 ZINC 2.
 FT METAL 163 163 ZINC 2.
 FT METAL 182 182 ZINC 2.
 FT METAL 185 185 ZINC 2.
 FT METAL 196 196 ZINC 1.
 FT METAL 199 199 ZINC 1.
 FT HELIX 5 8
 FT TURN 9 10
 FT TURN 13 14
 FT HELIX 18 31
 FT TURN 32 35
 FT HELIX 36 38
 FT TURN 41 42
 FT HELIX 43 50
 FT TURN 51 51
 FT HELIX 52 56
 FT HELIX 59 64
 FT HELIX 65 67
 FT TURN 68 73
 FT TURN 131 133
 FT STRAND 140 142
 FT HELIX 144 146
 FT TURN 147 149
 FT STRAND 151 151
 FT STRAND 158 159
 FT TURN 161 165
 FT STRAND 168 173
 FT TURN 174 175
 FT STRAND 176 181
 FT TURN 183 187
 FT STRAND 190 191
 FT STRAND 195 195
 FT HELIX 197 199
 FT TURN 200 201
 FT TURN 204 206
 SQ SEQUENCE 375 AA; 40969 MW; 8DE1863CC0BD8C3F CRC64;
 Query Match 100.0%; Score 81; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 7.4e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 60 QKRAVDQYGHAF 74
 QY 1 QKRAVDQYGHAF 15
 DB 60 QKRAVDQYGHAF 74
 RESULT 2
 ID DnaJ_HAEDU STANDARD; PRT; 377 AA.
 AC P48208;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Chaperone protein dnaJ.
 GN DnaJ OR HD0188.
 OS Haemophilus ducreyi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=35000HP / ATCC 700724;
 RA Parsons L.M.;
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=35000HP / ATCC 700724;
 RA Johnson R.S., Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
 RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
 RT "The complete genome sequence of Haemophilus ducreyi.";
 RT Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with GRPE,


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CC the ATPase activity of dnaK (By similarity).
CC -1- COPACITOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 J domain.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -----
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CC -----
DR EMBL; U25996; AAA67299.1; -.
DR EMBL; AB017151; AAP95181.1; -.
DR HSSP; P08622; 1BQZ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
KW Complete proteome.
FT DOMAIN 3 72 J-DOMAIN.
FT REPEAT 147 108 GLY-RICH.
FT REPEAT 147 154 CXXCXGKG MOTIF.
FT REPEAT 164 171 CXXCXGKG MOTIF.
FT REPEAT 186 193 CXXCXGKG MOTIF.
FT REPEAT 200 207 CXXCXGKG MOTIF.
FT METAL 147 147 ZINC 1 (BY SIMILARITY).
FT METAL 150 150 ZINC 1 (BY SIMILARITY).
FT METAL 164 164 ZINC 2 (BY SIMILARITY).
FT METAL 167 167 ZINC 2 (BY SIMILARITY).
FT METAL 186 186 ZINC 2 (BY SIMILARITY).
FT METAL 189 189 ZINC 2 (BY SIMILARITY).
FT METAL 200 200 ZINC 1 (BY SIMILARITY).
FT METAL 203 203 ZINC 1 (BY SIMILARITY).
SQ SEQUENCE 377 AA; 41027 MW; 37E9048F81A1A7A9 CRC64;
Query Match 100.0%; Score 81; DR 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 7,4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAE 15
Db 61 QKRAAYDQYGHAAE 75
RESULT 3
DnaJ_SALT
ID DnaJ_SALT STANDARD; PRT; 378 AA.
AC 060004;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chaperone protein dnaJ.
DE DnaJ OR STM0013 OR STY0013 OR T0013.
OS Salmonella typhimurium, and
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RP [1]
SEQUENCE FROM N.A.
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RC SPECIES=S.typhimurium; STRAIN=LT2;
RA Stephen R.J., Hinton J.C.D.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700120;
RX MEDLINE=21534948; PubMed=11677609;
RA McCelland M., Sanderson K.E., Spieth U., Clifton S.W., Latreille P.,
RA Courtney L., Powellik S., Ali U., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford S., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Lion S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: INTERACTS WITH DnaK. TO DISASSEMBLE A PROTEIN COMPLEX
CC AT THE PHASE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY
CC WITH GRP, THE ATPASE ACTIVITY OF DnaK.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- INDUCTION: BY HEAT SHOCK UNDER THE CONTROL OF THE HSPR REGULATORY
CC PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 J domain.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -----
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CC -----
DR EMBL; U58360; AAB02911.1; -.
DR EMBL; AB008693; AAL18977.1; -.
DR EMBL; AL627265; CAD01166.1; -.
DR EMBL; AB016834; AAO67747.1; -.
DR HSSP; P08622; 1EXK.
DR StyGene; SG10620; dnaJ.
DR InterPro; IPR002938; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
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DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DNAJ_1; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
DR PROSITE; PS00637; DNAJ_CXXCXGK; 1.
KM Chapterone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
KW Complete proteome.
FT INIT_MET 0 BY SIMILARITY.
FT DOMAIN 2 71 U-DOMAIN.
FT DOMAIN 76 112 GLY-RICH.
FT REPEAT 146 153 CXXCXGK MOTIF.
FT REPEAT 163 170 CXXCXGK MOTIF.
FT REPEAT 185 192 CXXCXGK MOTIF.
FT REPEAT 199 206 CXXCXGK MOTIF.
FT METAL 146 146 ZINC 1 (BY SIMILARITY).
FT METAL 149 149 ZINC 1 (BY SIMILARITY).
FT METAL 163 163 ZINC 2 (BY SIMILARITY).
FT METAL 166 166 ZINC 2 (BY SIMILARITY).
FT METAL 185 185 ZINC 2 (BY SIMILARITY).
FT METAL 188 188 ZINC 2 (BY SIMILARITY).
FT METAL 199 199 ZINC 1 (BY SIMILARITY).
FT METAL 202 202 ZINC 1 (BY SIMILARITY).
SQ SEQUENCE 378 AA; 41181 MW; 176EEC64696F30A2 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAYDQYGHAF 15
Db 60 QKRAYDQYGHAF 74
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|

RESULT 4
DNAJ_HABIN STANDARD; PRT; 382 AA.
AC P43735;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chapterone protein dnaJ.
GN DNAJ OR H11238.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kitzness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uitterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd."
RL Science 269:496-512(1995).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -----
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CC -----
DR EMBL; U32803; AAC22890.1; ALT_INIT.
DR HSSP; P08622; 1BQZ.
DR TIGR; H11238; -.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGK.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hep_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGK; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DNAJ_1; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
DR PROSITE; PS00637; DNAJ_CXXCXGK; 1.
KM Chapterone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
KW Complete proteome.
FT INIT_MET 3 72 U-DOMAIN.
FT DOMAIN 77 110 GLY-RICH.
FT REPEAT 147 154 CXXCXGK MOTIF.
FT REPEAT 164 171 CXXCXGK MOTIF.
FT REPEAT 186 193 CXXCXGK MOTIF.
FT REPEAT 200 207 CXXCXGK MOTIF.
FT METAL 147 147 ZINC 1 (BY SIMILARITY).
FT METAL 150 150 ZINC 1 (BY SIMILARITY).
FT METAL 164 164 ZINC 2 (BY SIMILARITY).
FT METAL 167 167 ZINC 2 (BY SIMILARITY).
FT METAL 186 186 ZINC 2 (BY SIMILARITY).
FT METAL 189 189 ZINC 2 (BY SIMILARITY).
FT METAL 200 200 ZINC 1 (BY SIMILARITY).
FT METAL 203 203 ZINC 1 (BY SIMILARITY).
SQ SEQUENCE 382 AA; 41222 MW; 8850B8B6FB2BC2B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAYDQYGHAF 15
Db 61 QKRAYDQYGHAF 75
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RESULT 5
DNAJ_ACTAC STANDARD; PRT; 375 AA.
AC P77866;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chapterone protein dnaJ.
GN DNAJ.
OS Actinobacillus actinomycetemcomitans (Haemophilus
OS actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y4;
RX MEDLINE=98182595; PubMed=9522128;
RA Yoshida A., Nakano Y., Yamashita Y., Yu H., Ohishi M., Koga T.,
RA "Isolation and characterization of the dnaJ operon from
RT Actinobacillus actinomycetemcomitans."
RT DNA Seq. 8:93-98(1997).
RL
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -----
```

CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 domain.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D87753; BAA32697.1; -
DR HSSP: P08622; 1BQZ.
DR InterPro: IPR002939; DnaJ_C.
DR InterPro: IPR001305; DnaJ_CXXCXGKG.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR008971; HSP40 DnaJ_pep.
DR InterPro: IPR003095; Hsp_DnaJ.
DR Pfam: PF00226; DnaJ_1.
DR Pfam: PF01556; DnaJ_C; 1.
DR Pfam: PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS: PR00625; DnaJPROTEIN.
DR SMART: SM00271; DnaJ; 1.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS0076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGKG; 1.
DR Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding.
KW DOMAIN.
FT DOMAIN 5 70
FT REPEAT 145 152 GLY-RICH.
FT REPEAT 162 169 CXXCXGKG MOTIF.
FT REPEAT 184 191 CXXCXGKG MOTIF.
FT REPEAT 198 205 CXXCXGKG MOTIF.
FT METAL 145 145 ZINC 1 (BY SIMILARITY).
FT METAL 148 148 ZINC 1 (BY SIMILARITY).
FT METAL 162 162 ZINC 2 (BY SIMILARITY).
FT METAL 165 165 ZINC 2 (BY SIMILARITY).
FT METAL 184 184 ZINC 2 (BY SIMILARITY).
FT METAL 187 187 ZINC 2 (BY SIMILARITY).
FT METAL 198 198 ZINC 1 (BY SIMILARITY).
FT METAL 201 201 ZINC 1 (BY SIMILARITY).
SQ SEQUENCE 375 AA; 41374 MW; CFPD286756FF4E1 CRC64;
Query Match 96.3%; Score 78; DB 1; Length 375;
Best Local Similarity 93.3%; Pred. No. 2.5e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 1 OKRAAYDYGHAAPF 15
Db 61 EKRAAYDYGHAAPF 75
RESULT 6
DnaJ_VIBCH STANDARD; PRT; 381 AA.
ID_DNAJ_VIBCH 034242; Q9KTP5; (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chaperone protein dnaJ.
GN DnaJ OR VC0856.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey R.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

RA Ermolaeva M.D., Vamathevan J., Baes S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utlacker T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RN Nature 406:477-483 (2000).
RL [2]
RP SEQUENCE OF 1-80 FROM N.A.
RC STRAIN=Classical 569B / ATCC 25870 / Serotype O1;
RX MEDLINE=99150229; PubMed=10024539;
RA Chakrabarti S., Sengupta N., Chowdhury R.;
RT "Role of DnaK in vitro and in vivo expression of virulence factors
RT of Vibrio cholerae.";
RL Infect. Immun. 67:1025-1033 (1999).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 domain.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE004171; AAF94018.1; -
DR EMBL: Y14237; CAI74628.1; -
DR PIR: D82270; D82270.
DR HSSP: P08622; 1BQZ.
DR TIGR: VC0856; -
DR InterPro: IPR002939; DnaJ_C.
DR InterPro: IPR001305; DnaJ_CXXCXGKG.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR008971; HSP40 DnaJ_pep.
DR InterPro: IPR003095; Hsp_DnaJ.
DR Pfam: PF00226; DnaJ_1.
DR Pfam: PF01556; DnaJ_C; 1.
DR Pfam: PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS: PR00625; DnaJPROTEIN.
DR SMART: SM00271; DnaJ; 1.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS0076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGKG; 1.
DR Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
KW Complete proteome.
FT DOMAIN 4 72
FT REPEAT 149 156 GLY-RICH.
FT REPEAT 166 173 CXXCXGKG MOTIF.
FT REPEAT 188 195 CXXCXGKG MOTIF.
FT REPEAT 202 209 CXXCXGKG MOTIF.
FT METAL 149 149 ZINC 1 (BY SIMILARITY).
FT METAL 152 152 ZINC 1 (BY SIMILARITY).
FT METAL 166 166 ZINC 2 (BY SIMILARITY).
FT METAL 169 169 ZINC 2 (BY SIMILARITY).
FT METAL 188 188 ZINC 2 (BY SIMILARITY).
FT METAL 191 191 ZINC 2 (BY SIMILARITY).
FT METAL 202 202 ZINC 1 (BY SIMILARITY).
FT METAL 205 205 ZINC 1 (BY SIMILARITY).
FT CONFLICT 37 38 NS -> TP (IN REF. 2).
FT CONFLICT 43 45 AAE -> CRG (IN REF. 2).
FT CONFLICT 49 51 EVK -> IQ (IN REF. 2).
FT CONFLICT 67 67 D -> E (IN REF. 2).
FT CONFLICT 71 71 H -> I (IN REF. 2).
FT CONFLICT 78 80 AGG -> RLV (IN REF. 2).
SQ SEQUENCE 381 AA; 40822 MW; 2188BE360D031505 CRC64;

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Query Match      Score 78;  DB 1;  Length 381;
Best Local Similarity 93.3%;
Matches 14;  Conservative 1;  Mismatches 0;  Indels 0;
QY      1 OKRAAYOYGHAAFE 15
        ||:|||||
        61 OKKAAYIDYGHAAFE 75

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DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Chaperone protein dnaJ.	
GN	dnaJ.	
OS	Vibrio harveyi.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	
OC	Vibrionaceae; Vibrio.	
OX	NCBI_TaxID=669;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=99418481; PubMed=9747709;	
RA	Klein G., Zmliwski M., Kzewska J., Czeczalka M., Lipinka B.,	
RT	"Cloning and characterization of the dnaK heat shock operon of the	
RT	marine bacterium Vibrio harveyi."	
RL	Mol. Gen. Genet. 259:179-189(1998).	
CC	-1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,	
CC	the ATPase activity of dnaK (By similarity).	
CC	-1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).	
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	
CC	-1- SIMILARITY: Belongs to the dnaJ family.	
CC	-1- SIMILARITY: Contains 1 J domain.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).	
CC	-----	
DR	EMBL, AF055368; AAC61693.1; --	
DR	HSSP, P08622; 1BQZ.	
DR	InterPro, IPR002939; DnaJ_C.	
DR	InterPro, IPR001305; DnaJ_CXKXGXG.	
DR	InterPro, IPR001623; DnaJ_N.	
DR	InterPro, IPR008971; HSP40_DnaJ_pep.	
DR	InterPro, IPR003095; Hsp_DnaJ.	
DR	Pfam, PF00226; DnaJ_1.	
DR	Pfam, PF01556; DnaJ_C_1.	
DR	Pfam, PF00684; DnaJ_CXKXGXG_1.	
DR	PRINTS, PR00625; DnaJPROTEIN.	
DR	SMART, SM00271; DnaJ_1.	
DR	PROSITE, PS00637; DnaJ_CXKXGXG_1.	
DR	PROSITE, PS00636; DnaJ_1_1.	
DR	PROSITE, PS0076; DnaJ_2_1.	
RW	Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding.	
FT	DOMAIN	5 70
FT	DOMAIN	77 120
FT	REPEAT	150 157
FT	REPEAT	167 174
FT	REPEAT	189 196
FT	REPEAT	202 209
FT	METAL	150 150
FT	METAL	153 153
FT	METAL	167 167
FT	METAL	170 170
FT	METAL	189 189
FT	METAL	192 192

Query Match	96.3%	Score 78;	DB 1;	Length 385;
Best Local Similarity	93.3%	Pred: No. 2.6e-06;		
Matches 1;	Conservative	1;	Mismatches 0;	Indels 0;
FT METAL	202	202	ZINC 1 (BY SIMILARITY) .	
FT METAL	205	205	ZINC 1 (BY SIMILARITY) .	
SQ SEQUENCE	385 AA;	41619 MM;	ABAI052321D15F58 CRC64;	

RESULT #	ID	STANDARD;	PRT;	234 AA.
1	DNAJ_RHILE			
2	DNAJ_RHILE			
3	033529;			
4	15-JUL-1998 (Rel. 36, Created)			
5	15-JUL-1998 (Rel. 36, last sequence update)			
6	16-OCT-2001 (Rel. 40, last annotation update)			
7	Chaperone protein dnaJ (Fragment).			
8	DNAJ.			
9	Rhizobium leguminosarum.			
10	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
11	Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.			
12	NCBI_TaxId=384;			
13	[1]			
14	SEQUENCE FROM N.A.			
15	STRAIN=8401.PRL1;			
16	Simpkins S.A., Johnston A.W.B., James R.;			
17	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.			
18	-1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,			
19	the ATPase activity of dnaK (By similarity).			
20	-1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).			
21	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
22	-1- SIMILARITY: Belongs to the dnaJ family.			
23	-1- SIMILARITY: Contains 1 J domain.			
24	-1- SIMILARITY: Contains 1 CR domain.			
25	-----			
26	CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
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31	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
32	CC or send an email to license@isb-sib.ch).			
33	CC -----			
34	DR EMBL; Y14649; CAA74983.1; -.			
35	DR HSPP; P08622; IBOZ.			
36	DR InterPro; IPR001305; DnaJ_CXXCXGXG.			
37	DR InterPro; IPR001623; DnaJ_N.			
38	DR InterPro; IPR008971; HSP40_DnaJ_pep.			
39	DR InterPro; IPR003095; Hsp_DnaJ.			
40	DR Pfam; PF00226; DnaJ; 1.			
41	DR PRINTS; PF00625; DnaJ_CXXCXGXG; 1.			
42	DR PRINTS; PR00625; DNAJPROTEIN.			
43	DR SMART; SM00271; DnaJ; 1.			
44	DR PROSITE; PS00636; DnaJ_1; 1.			
45	DR PROSITE; PS00076; DnaJ_2; 1.			
46	DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.			
47	Kw Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding.			
48	FT DOMAIN 3 72			
49	FT DOMAIN 77 119			
50	FT REPEAT 149 156			
51	FT REPEAT 166 173			
52	FT REPEAT 188 195			
53	FT REPEAT 202 209			
54	FT METAL 149 149			
55	FT METAL 152 152			
56	FT METAL 166 166			
57	FT METAL 169 169			
58	FT METAL 188 188			
59	FT METAL 191 191			
60	FT METAL 191 191			
61	FT METAL 191 191			
62	FT METAL 191 191			
63	FT METAL 191 191			
64	FT METAL 191 191			
65	FT METAL 191 191			
66	FT METAL 191 191			
67	FT METAL 191 191			
68	FT METAL 191 191			
69	FT METAL 191 191			
70	FT METAL 191 191			
71	FT METAL 191 191			
72	FT METAL 191 191			
73	FT METAL 191 191			
74	FT METAL 191 191			
75	FT METAL 191 191			
76	FT METAL 191 191			
77	FT METAL 191 191			
78	FT METAL 191 191			
79	FT METAL 191 191			
80	FT METAL 191 191			
81	FT METAL 191 191			
82	FT METAL 191 191			
83	FT METAL 1			

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QY      1 QKRAAYDQYGHAAFE 15
          |||||:|||||
Db      60 QKRAAYDRYGHAAFE 74
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SEQ	SEQUENCE	372 AA:	40776 MM:	339B5FE13721DA9 CR664
FT	DOMAIN	77	114	U-DOMAIN.
FT	REPEAT	143	150	GLU-RICH.
FT	REPEAT	160	167	CCXXCXG MOTIF.
FT	REPEAT	182	189	CCXXCXG MOTIF.
FT	REPEAT	196	203	CCXXCXG MOTIF.
FT	METAL	143	143	ZINC 1 (BY SIMILARITY).
FT	METAL	146	146	ZINC 1 (BY SIMILARITY).
FT	METAL	160	160	ZINC 2 (BY SIMILARITY).
FT	METAL	163	163	ZINC 2 (BY SIMILARITY).
FT	METAL	182	182	ZINC 2 (BY SIMILARITY).
FT	METAL	185	185	ZINC 2 (BY SIMILARITY).
FT	METAL	196	196	ZINC 1 (BY SIMILARITY).
FT	METAL	199	199	ZINC 1 (BY SIMILARITY).

Query Match	92.6%	Score 75:	DB 1:	Length 372;
Best Local Similarity	93.3%	Pred:	8.4e-06;	
Matches 14:	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

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QY      1 OKRAAYDOYGHAAFE 15
Db      61 OKRAAYDOYGHAAFE 75

RESULT 11
ID      DNAME_BUCAL STANDARD; PRT: 377 AA.
AC      O32465;
DT      30-MAY-2000 (Rel. 39, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Chaparone protein dnaJ.
GN      DNAME OR B0152.
OS      Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OC      symbiotic bacterium).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Buchnera.
OX      NCBI_TaxID=118099;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97420684; PubMed=9276669;
RA      Sato S., Ishikawa H.;
RT      "Structure and expression of the dnaJ operon of Buchnera, an
RL      intracellular symbiotic bacteria of aphid.";
RL      J. Biochem. 122:41-48(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=Tokyo 1998;
RX      MEDLINE=20445173; PubMed=10993077;
RA      Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT      "Genome sequence of the endocellular bacterial symbiont of aphids
RL      Buchnera sp. APS.";
RL      Nature 407:81-86(2000).
CC      -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC      the ATPase activity of dnaK (By similarity).
CC      -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC      -1- SIMILARITY: Belongs to the dnaJ family.
CC      -1- SIMILARITY: Contains 1 CR domain.
CC      -1- SIMILARITY: Contains 1 CR domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; D86673; BAA21965.1; -.
DR      EMBL; AP001118; BAB12870.1; -.
DR      HSSP; P08622; 1BQZ.
DR      InterPro; IPR002939; DnaJ_C.
DR      InterPro; IPR001305; DnaJ_CXXCXXG.
DR      InterPro; IPR001623; DnaJ_N.
DR      InterPro; IPR008971; HSP40_DnaJ_pep.
DR      InterPro; IPR003095; Hsp_DnaJ.
DR      Pfam; PF00226; DnaJ; 1.
DR      Pfam; PF01556; DnaJ_C; 1.
DR      Pfam; PF00684; DnaJ_CXXCXXG; 1.
DR      PRINTS; PR00625; DNAMEPROTEIN.
DR      SMART; SM00271; DnaJ; 1.
DR      PROSITE; PS00636; DNAME_1; 1.
DR      PROSITE; PS0076; DNAME_2; 1.
DR      PROSITE; PS00637; DNAME_CXXCXXG; FALSE_NEG.
KM      Chaparone, DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
KM      Complete proteome.
FT      DOMAIN 5 70 1-DOMAIN.
FT      DOMAIN 77 115 GUY-RICH.
FT      REPEAT 145 152 CXXCXXG MOTIF.
FT      REPEAT 162 169 CXXCXXG MOTIF.

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FT      REPEAT 184 191 CXXCXXG MOTIF.
FT      REPEAT 198 205 CXXCXXG MOTIF.
FT      METAL 145 145 ZINC 1 (BY SIMILARITY).
FT      METAL 148 148 ZINC 1 (BY SIMILARITY).
FT      METAL 162 162 ZINC 2 (BY SIMILARITY).
FT      METAL 165 165 ZINC 2 (BY SIMILARITY).
FT      METAL 184 184 ZINC 2 (BY SIMILARITY).
FT      METAL 187 187 ZINC 2 (BY SIMILARITY).
FT      METAL 198 198 ZINC 1 (BY SIMILARITY).
FT      METAL 201 201 ZINC 1 (BY SIMILARITY).
FT      CONFLICT 185 185 P -> S (IN REF. 1).
FT      CONFLICT 270 270 I -> K (IN REF. 1).
SQ      SEQUENCE 377 AA; 42344 MW; F232B95530CC298B CRC64;

Query Match 92.6%; Score 75; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 8.5e-06;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 OKRAAYDOYGHAAFE 15
Db      61 OKRAAYDOYGHAAFE 75

RESULT 12
ID      DNAME_BUCAP STANDARD; PRT: 378 AA.
AC      OKR979;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Chaparone protein dnaJ.
GN      DNAME OR B053145.
OS      Buchnera aphidicola (subsp. Schizaphis graminum).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Buchnera.
OX      NCBI_TaxID=98794;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22084549; PubMed=12089438;
RA      Tamás I., Klasson L., Canback B., Naeslund A.K., Eriksson A.-S.,
RA      Wernegreen U.J., Sandstrom U.P., Moran N.A., Andersson S.G.E.;
RT      "50 million years of genomic stasis in endosymbiotic bacteria.";
RL      Science 296:2376-2379(2002).
CC      -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC      the ATPase activity of dnaK (By similarity).
CC      -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC      -1- SIMILARITY: Belongs to the dnaJ family.
CC      -1- SIMILARITY: Contains 1 CR domain.
CC      -1- SIMILARITY: Contains 1 CR domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AE014090; AAM67713.1; -.
DR      InterPro; IPR002939; DnaJ_C.
DR      InterPro; IPR001305; DnaJ_CXXCXXG.
DR      InterPro; IPR001623; DnaJ_N.
DR      InterPro; IPR008971; HSP40_DnaJ_pep.
DR      InterPro; IPR003095; Hsp_DnaJ.
DR      Pfam; PF00226; DnaJ; 1.
DR      Pfam; PF01556; DnaJ_C; 1.
DR      Pfam; PF00684; DnaJ_CXXCXXG; 1.
DR      PRINTS; PR00625; DNAMEPROTEIN.
DR      SMART; SM00271; DnaJ; 1.
DR      PROSITE; PS00636; DNAME_1; 1.
DR      PROSITE; PS0076; DNAME_2; 1.

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DR PROSITE; PS00637; DnaJ CXXCXGKG; FALSE NEG.
 KW Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
 Complete proteome.

FT	DOMAIN	5	70
FT	DOMAIN	77	116
FT	REPEAT	146	153
FT	REPEAT	163	170
FT	REPEAT	185	192
FT	REPEAT	199	206
FT	METAL	146	146
FT	METAL	149	149
FT	METAL	163	163
FT	METAL	166	166
FT	METAL	185	185
FT	METAL	188	188
FT	METAL	199	199
FT	METAL	202	202
SQ	SEQUENCE	378 AA;	42469 MW; BB73F48DAF7AD34 CRC64;

Query Match 91.4%; Score 74; DB 1; Length 378;
 Best Local Similarity 86.7%; Pred. No. 1.3e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAYDQYGHAF 15
 :||| ||||| |||||
 Db 61 EKRAYDQYGHAF 75

RESULT 13
 ID DnaJ_NEIMA STANDARD; PRT; 373 AA.
 AC P51707;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chaperone protein dnat.
 GN DnaJ OR NMA0209 OR NMB0059.
 OS Neisseria meningitidis (serogroup A), and
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_TaxID=65699, 491;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Z2491 / Serogroup A / Serotype 4A;
 RC MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
 RA Jørgels K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis Z2491."
 RT Nature 404:502-506(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MC58 / Serogroup B;
 RC MEDLINE=20175755; PubMed=10710307;
 RA Tettein H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwyn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Hatt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,
 RA Colton M.D., Uterback T.R., Khouri H., Qin H., Vamshdevan J.,
 RA Gill J., Scarlato V., Masigiani V., Piza M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58."
 RT Science 287:1809-1815(2000).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
 CC the ATPase activity of dnaJ (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -----
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 CC -----
 DR EMBL; AL162752; CAB83522.1; -
 DR EMBL; AE002365; AAP40528.1; -
 DR PIR; D81242; D81242.
 DR HSP; P08622; H8QZ.
 DR TIGR; NMB0059; -
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pep.
 DR InterPro; IPR003095; Hsp_DnaJ.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS00766; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
 Complete proteome.

FT	DOMAIN	5	70
FT	DOMAIN	76	117
FT	REPEAT	147	154
FT	REPEAT	164	171
FT	REPEAT	186	193
FT	REPEAT	200	207
FT	METAL	147	147
FT	METAL	150	150
FT	METAL	164	164
FT	METAL	167	167
FT	METAL	186	186
FT	METAL	189	189
FT	METAL	200	200
FT	METAL	203	203
SQ	SEQUENCE	373 AA;	40585 MW; 4D81E20A5D831CF CRC64;

Query Match 90.1%; Score 73; DB 1; Length 373;
 Best Local Similarity 86.7%; Pred. No. 1.9e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QKRAYDQYGHAF 15
 :||| ||||| |||||
 Db 61 EKRAYDQYGHAF 75

RESULT 14
 ID DnaJ_BRUV STANDARD; PRT; 375 AA.
 AC Q05980;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chaperone protein dnat.
 GN DnaJ.
 OS Brucella ovis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Brucellaceae; Brucella.
 NCBI_TaxID=236;
 [1]
 RN SEQUENCE FROM N.A.

RC STRAIN=ATCC 25840 / 63/290T;
 RX MEDLINE=93094135; PubMed=145952;
 RA Cellier M.F.M., Teyssier J., Nicolas M., Liautard J.P., Marti J.,
 RT "Cloning and characterization of the *Brucella ovis* heat shock protein
 RT dnaK functionally expressed in *Escherichia coli*.";
 RL J. Bacteriol. 174:8036-8042 (1992).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- INDUCTION: By heat shock.
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 CR domain.
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 CC -----
 CC EMBL: M95799; AAC36133.1; -.
 CC PIR: B47042; B47042.
 CC HSSP: P08622; 1B0Z.
 CC InterPro: IPR002939; DnaJ_C.
 CC InterPro: IPR001305; DnaJ_CXXCXGKG.
 CC InterPro: IPR001623; DnaJ_N.
 CC InterPro: IPR008971; HSP40_DnaJ_pdp.
 CC InterPro: IPR003095; Hsp_DnaJ.
 CC Pfam: PF00226; DnaJ_1.
 CC Pfam: PF01556; DnaJ_C_1.
 CC Pfam: PF00684; DnaJ_CXXCXGKG; 1.
 CC PRINTS: PR00625; DNAPROTEIN.
 CC SMART: SMO0271; DnaJ_1.
 CC PROSITE: PS00636; DnaJ_1; 1.
 CC PROSITE: PS0076; DnaJ_2; 1.
 CC PROSITE: PS00637; DnaJ_CXXCXGKG; 1.
 CC Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding.
 CC J-DOMAIN.
 CC FT DOMAIN 4 69
 CC FT REPEAT 146 106 GYX-RICH.
 CC FT REPEAT 163 153 CXXCXGKG MOTIF.
 CC FT REPEAT 185 170 CXXCXGKG MOTIF.
 CC FT REPEAT 199 192 CXXCXGKG MOTIF.
 CC FT REPEAT 206 206 CXXCXGKG MOTIF.
 CC FT METAL 146 146 ZINC 1 (BY SIMILARITY).
 CC FT METAL 149 149 ZINC 1 (BY SIMILARITY).
 CC FT METAL 163 163 ZINC 2 (BY SIMILARITY).
 CC FT METAL 166 166 ZINC 2 (BY SIMILARITY).
 CC FT METAL 185 185 ZINC 2 (BY SIMILARITY).
 CC FT METAL 188 188 ZINC 2 (BY SIMILARITY).
 CC FT METAL 199 199 ZINC 1 (BY SIMILARITY).
 CC FT METAL 202 202 ZINC 1 (BY SIMILARITY).
 CC SEQUENCE 375 AA; 41021 MW; 61CB5F99FA2DC73D CRC64;
 Query Match 90.1%; Score 73; DB 1; Length 375;
 Best Local Similarity 86.7%; Pred. No. 1.9e-05;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DE Chaperone protein dnaJ.
 GN DnaJ OR ATU0121 OR AGR_C 192.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 CC Ncbi_TaxId=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D., St.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krepan M., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neeter E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Ouxolli B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Hummel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58";
 RL Science 294:2323-2328 (2001).
 RN [3]
 RP SEQUENCE OF 1-66 FROM N.A.
 RX MEDLINE=96011387; PubMed=7592349;
 RA Segal G., Ron E.Z.;
 RT "The dnaJ operon of Agrobacterium tumefaciens: transcriptional
 RT analysis and evidence for a new heat shock promoter.";
 RL J. Bacteriol. 177:5952-5958 (1995).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- INDUCTION: By heat shock.
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 CC -1- SIMILARITY: Contains 1 CR domain.
 CC -1- SIMILARITY: Contains 1 CR domain.
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 CC -----
 CC EMBL: AE008986; AA141146.1; -.
 CC EMBL: AE007953; AA085941.1; -.
 CC EMBL: X87113; CAA60593.1; -.
 CC PIR: AD2591; AD2591.
 CC PIR: D97373; D97373.
 CC PIR: I39586; I39586.
 CC HSSP: P08622; 1B0Z.
 CC InterPro: IPR002939; DnaJ_C.
 CC InterPro: IPR001305; DnaJ_CXXCXGKG.
 CC InterPro: IPR001623; DnaJ_N.
 CC InterPro: IPR003095; Hsp_DnaJ.
 CC Pfam: PF00226; DnaJ_1.
 CC Pfam: PF01556; DnaJ_C_1.
 CC Pfam: PF00684; DnaJ_CXXCXGKG; 1.
 CC PRINTS: PR00625; DNAPROTEIN.

DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KM Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-Binding;
Complete proteome.
FT DOMAIN 5 70 J-DOMAIN.
FT DOMAIN 77 109 GLY-RICH.
FT REPEAT 151 158 CXXCXGXG MOTIF.
FT REPEAT 168 175 CXXCXGXG MOTIF.
FT REPEAT 190 197 CXXCXGXG MOTIF.
FT REPEAT 204 211 CXXCXGXG MOTIF.
FT METAL 151 151 ZINC 1 (BY SIMILARITY).
FT METAL 154 154 ZINC 1 (BY SIMILARITY).
FT METAL 168 168 ZINC 2 (BY SIMILARITY).
FT METAL 171 171 ZINC 2 (BY SIMILARITY).
FT METAL 190 190 ZINC 2 (BY SIMILARITY).
FT METAL 193 193 ZINC 2 (BY SIMILARITY).
FT METAL 204 204 ZINC 1 (BY SIMILARITY).
FT METAL 207 207 ZINC 1 (BY SIMILARITY).
FT CONFLICT 4 4 A -> R (IN REF. 3).
SQ SEQUENCE 377 AA; 40894 MW; 0E68A1D30754D18A CRC64;

Query Match 90.1%; Score 73; DB 1; Length 377;
Best Local Similarity 86.7%; Pred. No. 1.9e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QKRAAYDQYGHAAFE 15
|||:|||:
Db 61 QKRAAYDRFGHAAFE 75

Search completed: August 17, 2004, 22:23:35
Job time : 14 secs

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